

Input file ftmzb48h10; Output File ftmzb48h10.pat
Sequence length 3637

GTCGACCCACGCGTCCGCACTCAACAATGCCTGCCCTCTCTGACTGCACCGTCCCGCCGCGCTGCCGCCGCGCGCC	79
CAAGCCAAGTCGAGCGGGGGCGTTGCCACCGACGGCACAGCCCTTGGGGCCCGCCCGGGACCAGGAGGTGAGCCGCGCG	158
CGCACAGCTCCGTGCGCTCGCCCGTCTGAGCGCCCGCCAGGTGCCCGCAGCCCGCGCGCGAG	233
ATG CAC AGC CCG	4
P G L L A L W L C A V L C A S A R G G S	24
CCT GGG CTC CTG GCG CTG TGG CTT TGC GCT GTG CTG TGC GCA TCG GCG CGC GGG GGC AGC	293
D P Q P G P G R P A C P A P C H C Q E D	44
GAC CCC CAG CCT GGC CCG GGG CGT CCC GCC TGC CCG GCT CCC TGC CAC TGC CAG GAG GAC	353
G I M L S A D C S E L G L S V V P A D L	64
GGC ATC ATG CTG TCC GCT GAC TGC TCC GAG CTC GGG CTC TCA GTG GTG CCT GCG GAC CTG	413
D P L T A Y L D L S M N N L T E L Q P G	84
GAC CCC CTG ACG GCT TAC CTA GAC CTC AGT ATG AAC AAC CTC ACG GAG CTT CAG CCG GGT	473
L F H H L R F L E E L R L S G N H L S H	104
CTC TTC CAC CAC CTG CGC TTC CTG GAG GAG CTG CGG CTC TCA GGG AAC CAC CTC TCA CAC	533
I P G Q A F S G L H S L K I L M L Q S N	124
ATC CCG GGA CAG GCA TTC TCC GGC CTC CAC AGC CTC AAA ATT CTA ATG CTG CAG AGC AAC	593
Q L R G I P A E A L W E L P S L Q S L R	144
CAG CTC CGT GGG ATC CCA GCA GAG GCA CTA TGG GAG CTG CCC AGC CTG CAG TCG CTG CGC	653
L D A N L I S L V P E R S F E G L S S L	164
CTA GAT GCT AAT CTC ATC TCC CTG GTC CCT GAG AGA AGC TTT GAG GGG CTC TCC TCC CTC	713
R H L W L D D N A L T E I P V R A L N N	184
CGC CAC CTC TGG CTG GAT GAC AAT GCA CTC ACT GAG ATC CCC GTC AGA GCT CTC AAC AAC	773
L P A L Q A M T L A L N H I R H I P D Y	204
CTT CCT GCC CTA CAG GCC ATG ACC TTG GCT CTC AAC CAT ATC CGC CAC ATC CCT GAC TAT	833
A F Q N L T S L V V L H L H N N R I Q H	224
GCC TTC CAG AAC CTC ACC AGT CTT GTG GTG CTG CAT CTA CAT AAC AAC CGC ATC CAG CAT	893
V G T H S F E G L H N L E T L D L N Y N	244
GTG GGG ACC CAC AGC TTC GAG GGG CTG CAC AAT CTG GAG ACA CTA GAC CTG AAC TAT AAT	953
E L Q E F P L A I R T L G R L Q E L G F	264
GAG CTG CAG GAG TTC CCC TTG GCT ATC CGG ACC CTG GGC AGG CTG CAG GAA TTG GGT TTC	1013
H N N N I K A I P E K A F M G N P L L Q	284
CAT AAC AAC AAC ATC AAG GCT ATC CCA GAG AAA GCC TTC ATG GGC AAC CCT CTC CTG CAG	1073
T I H F Y D N P I Q F V G R S A F Q Y L	304
ACA ATA CAT TTT TAT GAC AAC CCA ATC CAG TTT GTG GGA AGG TCA GCA TTC CAG TAC CTG	1133
S K L H T L S L N G A T D I Q E F P D L	324
TCT AAA CTG CAT ACG CTA TCT TTG AAT GGT GCC ACT GAT ATC CAA GAG TTC CCA GAC CTC	1193
K G T T S L E I L T L T R A G I R L L P	344
AAA GGC ACC ACT AGC CTG GAG ATC CTG ACC CTG ACC CGT GCG GGC ATC AGA CTG CTC CCA	1253

Figure 1

LRR: domain 1 of 8, from 67 to 114: score 46.0, E = 8.1e-10

->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnlk<-
+LdLs N+Lt+lpg++++L+ LeeL Ls+N+L+++p +++f++L+

ftmzb048h1

67 LTAYLDLSMNNLTQLPGLFHHLRFLEELRLSGNHLSHIPGQAFSGLH 114

LRR: domain 2 of 8, from 115 to 162: score 42.2, E = 1.2e-08

->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnlk<-
+L+ L L+ N+L+++p++al+ Lp+L++L L+ N ++ +p+++f++L+

ftmzb048h1

115 SLKILMLQSNQLRGIPAEALWELPSLQSLRLDANLISLVPERSFEGLS 162

LRR: domain 3 of 8, from 163 to 210: score 49.5, E = 7.7e-11

->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnlk<-
+L++L+L++N Lt++p al+nLp L+ L N+++++p+++fqnl+

ftmzb048h1

163 SLRHLWLDNALTEIPVRALNNLPALQAMTLALNHIRHIPDYAFQNL 210

LRR: domain 4 of 8, from 211 to 257: score 39.5, E = 7.4e-08

->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnlk<-
+L+L+L nN+++++ +++++L+nLe+LdL++N+L+++p ++L+

ftmzb048h1

211 SLVVLHLHNNRIQHVGHHSFEGHLNLETDLNYNELQEFPL-AIRTLG 257

LRR: domain 5 of 8, from 258 to 305: score 34.1, E = 3.2e-06

->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnlk<-
+L+eL + nN+++ +p+ at + p L+++++ +N ++ + ++fq L+

ftmzb048h1

258 RLQELGFHNNNIKAPEKAFMGNPLLQTIHFYDNPIQFVGRSAFQYLS 305

LRR: domain 6 of 8, from 306 to 352: score 23.8, E = 0.0041

->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnlk<-
+L++L+L++ +++++p+ l++ ++Le L L + ++ lppg++q L+

ftmzb048h1

306 KLHTLSLNGATdIQEFPD-LKGTTSLEILTLTRAGIRLLPPGVCQQLP 352

LRR: domain 7 of 8, from 353 to 398: score 47.6, E = 2.8e-10

->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnlk<-
+L+ L+Ls+N++++lp+ l+ +++Lee+ L +N+++++ ++f+ L+

ftmzb048h1

353 RLRILELSHNQIEELPS-LHRCQKLEEIGLRHNRKEIGADTFSQLG 398

LRR: domain 8 of 8, from 399 to 446: score 49.4, E = 7.9e-11

->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnlk<-
+L+ LdLs N ++ ++p+a+s+L++L +LdL +N+Lt+lp + +L

ftmzb048h1

399 SLQALDLSWNAIRAIHPEAFSTLRSLVKLDLTDNQLTTPLAGLGGLM 446

Figure 2

[illegible]

Figure 3

[illegible]

Figure 4

—

[illegible]

Figure 5

LRR: domain 1 of 1, from 64 to 111: score 51.0, E = 2.6e-11

*->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnl

+L+ LdLs N ++s++p+a+s+L++L +LdL +N+Lt+lp + +L

fahr 64 SLQALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTPLAGLGGL 110

k<*

fahr 111 M 111

Figure 6

G	L	H	N	L	E	T	L	D	L	N	Y	N	K	L	Q	E	F	P	V	20
GGG	CTG	CAC	AAT	CTG	GAG	ACA	CTA	GAC	CTG	AAT	TAT	AAC	AAG	CTG	CAG	GAG	TTC	CCT	GTG	60
A	I	R	T	L	G	R	L	Q	E	L	G	F	H	N	N	N	I	K	A	40
GCC	ATC	CGG	ACC	CTG	GGC	AGA	CTG	CAG	GAA	CTG	GGG	TTC	CAT	AAC	AAC	AAC	ATC	AAG	GCC	120
I	P	E	K	A	F	M	G	N	P	L	L	Q	T	I	H	F	Y	D	N	60
ATC	CCA	GAA	AAG	GCC	TTC	ATG	GGG	AAC	CCT	CTG	CTA	CAG	ACG	ATA	CAC	TTT	TAT	GAT	AAC	180
P	I	Q	F	V	G	R	S	A	F	Q	Y	L	P	K	L	H	T	L	S	80
CCA	ATC	CAG	TTT	GTG	GGA	AGA	TCG	GCA	TTC	CAG	TAC	CTG	CCT	AAA	CTC	CAC	ACA	CTA	TCT	240
L	N	G	A	M	D	I	Q	E	F	P	D	L	K	G	T	T	S	L	E	100
CTG	AAT	GGT	GCC	ATG	GAC	ATC	CAG	GAG	TTT	CCA	GAT	CTC	AAA	GGC	ACC	ACC	AGC	CTG	GAG	300
I	L	T	L	T	R	A	G	I	R	L	L	P	S	G	M	C	Q	Q	L	120
ATC	CTG	ACC	CTG	ACC	CGC	GCA	GGC	ATC	CGG	CTG	CTC	CCA	TCG	GGG	ATG	TGC	CAA	CAG	CTG	360
P	R	L	R	V	L	E	L	S	H	N	Q	I	E	E	L	P	S	L	H	140
CCC	AGG	CTC	CGA	GTC	CTG	GAA	CTG	TCT	CAC	AAT	CAA	ATT	GAG	GAG	CTG	CCC	AGC	CTG	CAC	420
R	C	Q	K	L	E	E	I	G	L	Q	H	N	R	I	W	E	I	G	A	160
AGG	TGT	CAG	AAA	TTG	GAG	GAA	ATC	GGC	CTC	CAA	CAC	AAC	CGC	ATC	TGG	GAA	ATT	GGA	GCT	480
D	T	F	S	Q	L	S	S	L	Q	A	L	D	L	S	W	N	A	I	R	180
GAC	ACC	TTC	AGC	CAG	CTG	AGC	TCC	CTG	CAA	GCC	CTG	GAT	CTT	AGC	TGG	AAC	GCC	ATC	CGG	540
S	I	H	P	E	A	F	S	T	L	H	S	L	V	K	L	D	L	T	D	200
TCC	ATC	CAC	CCT	GAG	GCC	TTC	TCC	ACC	CTG	CAC	TCC	CTG	GTC	AAG	CTG	GAC	CTG	ACA	GAC	600
N	Q	L	T	T	L	P	L	A	G	L	G	G	L	M	H	L	K	L	K	220
AAC	CAG	CTG	ACC	ACA	CTG	CCC	CTG	GCT	GGA	CTT	GGG	GGC	TTG	ATG	CAT	CTG	AAG	CTC	AAA	660
G	N	L	A	L	S	Q	A	F	S	K	D	S	F	P	K	L	R	I	L	240
GGG	AAC	CTT	GCT	CTC	TCC	CAG	GCC	TTC	TCC	AAG	GAC	AGT	TTC	CCA	AAA	CTG	AGG	ATC	CTG	720
E	V	P	Y	A	Y	Q	C	C	P	Y	G	M	C	A	S	F	F	K	A	260
GAG	GTG	CCT	TAT	GCC	TAC	CAG	TGC	TGT	CCC	TAT	GGG	ATG	TGT	GCC	AGC	TTC	TTC	AAG	GCC	780
S	G	Q	W	E	A	E	D	L	H	L	D	D	E	E	S	S	K	R	P	280
TCT	GGG	CAG	TGG	GAG	GCT	GAA	GAC	CTT	CAC	CTT	GAT	GAT	GAG	GAG	TCT	TCA	AAA	AGG	CCC	840
L	G	L	L	A	R	Q	A	E	N	H	Y	D	Q	D	L	D	E	L	Q	300
CTG	GGC	CTC	CTT	GCC	AGA	CAA	GCA	GAG	AAC	CAC	TAT	GAC	CAG	GAC	CTG	GAT	GAG	CTC	CAG	900
L	E	M	E	D	S	K	P	H	P	S	V	Q	C	S	P	T	P	G	P	320
CTG	GAG	ATG	GAG	GAC	TCA	AAG	CCA	CAC	CCC	AGT	GTC	CAG	TGT	AGC	CCT	ACT	CCA	GGC	CCC	960
F	K	P	C	E	Y	L	F	E	S	W	G	I	R	L	A	V	W	A	I	340
TTC	AAG	CCC	TGT	GAG	TAC	CTC	TTT	GAA	AGC	TGG	GGC	ATC	CGC	CTG	GCC	GTG	TGG	GCC	ATC	1020
V	L	L	S	V	L	C	N	G	L	V	L	L	T	V	F	A	G	G	P	360
GTG	TTG	CTC	TCC	GTG	CTC	TGC	AAT	GGA	CTG	GTG	CTG	CTG	ACC	GTG	TTC	GCT	GGC	GGG	CCT	1080
A	P	L	P	P	V	K	F	V	V	G	A	I	A	G	A	N	T	L	T	380
GCC	CCC	CTG	CCC	CCG	GTC	AAG	TTT	GTG	GTA	GGT	GCG	ATT	GCA	GGC	GCC	AAC	ACC	TTG	ACT	1140

FIGURE 8

G	I	S	C	G	L	L	A	S	V	D	A	L	T	F	G	Q	F	S	E	400
GGC	ATT	TCC	TGT	GGC	CTT	CTA	GCC	TCA	GTC	GAT	GCC	CTG	ACC	TTT	GGT	CAG	TTC	TCT	GAG	1200
Y	G	A	R	W	E	T	G	L	G	C	R	A	T	G	F	L	A	V	L	420
TAC	GGA	GCC	CGC	TGG	GAG	ACG	GGG	CTA	GGC	TGC	CGG	GCC	ACT	GGC	TTC	CTG	GCA	GTA	CTT	1260
G	S	E	A	S	V	L	L	L	T	L	A	A	V	Q	C	S	V	S	V	440
GGG	TCG	GAG	GCA	TCG	GTG	CTG	CTG	CTC	ACT	CTG	GCC	GCA	GTG	CAG	TGC	AGC	GTC	TCC	GTC	1320
S	C	V	R	A	Y	G	K	S	P	S	L	G	S	V	R	A	G	V	L	460
TCC	TGT	GTC	CGG	GCC	TAT	GGG	AAG	TCC	CCC	TCC	CTG	GGC	AGC	GTT	CGA	GCA	GGG	GTC	CTA	1380
G	C	L	A	L	A	G	L	A	A	A	L	P	L	A	S	V	G	E	Y	480
GGC	TGC	CTG	GCA	CTG	GCA	GGG	CTG	GCC	GCC	GCA	CTG	CCC	CTG	GCC	TCA	GTG	GGA	GAA	TAC	1440
G	A	S	P	L	C	L	P	Y	A	P	P	E	G	Q	P	A	A	L	G	500
GGG	GCC	TCC	CCA	CTC	TGC	CTG	CCC	TAC	GCG	CCA	CCT	GAG	GGT	CAG	CCA	GCA	GCC	CTG	GGC	1500
F	T	V	A	L	V	M	M	N	S	F	C	F	L	V	V	A	G	A	Y	520
TTC	ACC	GTG	GCC	CTG	GTG	ATG	ATG	AAC	TCC	TTC	TGT	TTC	CTG	GTC	GTG	GCC	GGT	GCC	TAC	1560
I	K	L	Y	C	D	L	P	R	G	D	F	E	A	V	W	D	C	A	M	540
ATC	AAA	CTG	TAC	TGT	GAC	CTG	CCG	CGG	GGC	GAC	TTT	GAG	GCC	GTG	TGG	GAC	TGC	GCC	ATG	1620
V	R	H	V	A	W	L	I	F	A	D	G	L	L	Y	C	P	V	A	F	560
GTG	AGG	CAC	GTG	GCC	TGG	CTC	ATC	TTC	GCA	GAC	GGG	CTC	CTC	TAC	TGT	CCC	GTG	GCC	TTC	1680
L	S	F	A	S	M	L	G	L	F	P	V	T	P	E	A	V	K	S	V	580
GTC	AGC	TTC	GCC	TCC	ATG	CTG	GGC	CTC	TTC	CCT	GTC	ACG	CCC	GAG	GCC	GTC	AAG	TCT	GTC	1740
L	L	V	V	L	P	L	P	A	C	L	N	P	L	L	Y	L	L	F	N	600
CTG	CTG	GTG	GTG	CTG	CCC	CTG	CCT	GCC	TGC	CTC	AAC	CCA	CTG	CTG	TAC	CTG	CTC	TTC	AAC	1800
P	H	F	R	D	D	L	R	R	L	R	P	R	A	G	D	S	G	P	L	620
CCC	CAC	TTC	CGG	GAT	GAC	CTT	CGG	CGG	CTT	CGG	CCC	CGC	GCA	GGG	GAC	TCA	GGG	CCC	CTA	1860
A	Y	A	A	A	G	E	L	E	K	S	S	C	D	S	T	Q	A	L	V	640
GCC	TAT	GCT	GCG	GCC	GGG	GAG	CTG	GAG	AAG	AGC	TCC	TGT	GAT	TCT	ACC	CAG	GCC	CTG	GTA	1920
A	F	S	D	V	D	L	I	L	E	A	S	E	A	G	R	P	P	G	L	660
GCC	TTC	TCT	GAT	GTG	GAT	CTC	ATT	CTG	GAA	GCT	TCT	GAA	GCT	GGG	CGG	CCC	CCT	GGG	CTG	1980
E	T	Y	G	F	P	S	V	T	L	I	S	C	Q	Q	P	G	A	P	R	680
GAG	ACC	TAT	GGC	TTC	CCC	TCA	GTG	ACC	CTC	ATC	TCC	TGT	CAG	CAG	CCA	GGG	GCC	CCC	AGG	2040
L	E	G	S	H	C	V	E	P	E	G	N	H	F	G	N	P	Q	P	S	700
CTG	GAG	GGC	AGC	CAT	TGT	GTA	GAG	CCA	GAG	GGG	AAC	CAC	TTT	GGG	AAC	CCC	CAA	CCC	TCC	2100
M	D	G	E	L	L	L	R	A	E	G	S	T	P	A	G	G	G	L	S	720
ATG	GAT	GGA	GAA	CTG	CTG	CTG	AGG	GCA	GAG	GGA	TCT	ACG	CCA	GCA	GGT	GGA	GGC	TTG	TCA	2160
G	G	G	G	F	Q	P	S	G	L	A	F	A	S	H	V	*				737
GGG	GGT	GGC	GGC	TTT	CAG	CCC	TCT	GGC	TTG	GCC	TTT	GCT	TCA	CAC	GTG	TAA				2211
ATATCCCTCCCCATTCTTCTCTTCCCCTCTCTTCCCTTTCCCTCTCTCCCCCTCGGTGAATGATGGCTGCTTCTAAAACA	2290																			
AATACAACCAAAACTCAGCAGTGTGATCTATAGCAGGATGGCCCAGTACCTGGCTCCACTGATCACCTCTCTCCTGTGA	2369																			
CCATCACCAACGGGTGCCTCTTGGCCTGGCTTTCCCTTGGCCTTCCTCAGCTTCACCTTGATACTGGGCCTCTTCCTTG	2448																			
TCATGTCTGAAGCTGTGGACCAGAGACCTGGACTTTTGTCTGCTTAAGGGAAATGAGGGAAGTAAAGACAGTGAAGGGG	2527																			

FIGURE 8

CONT.

[illegible]

FIGURE 8
CONT.

100000 3634300

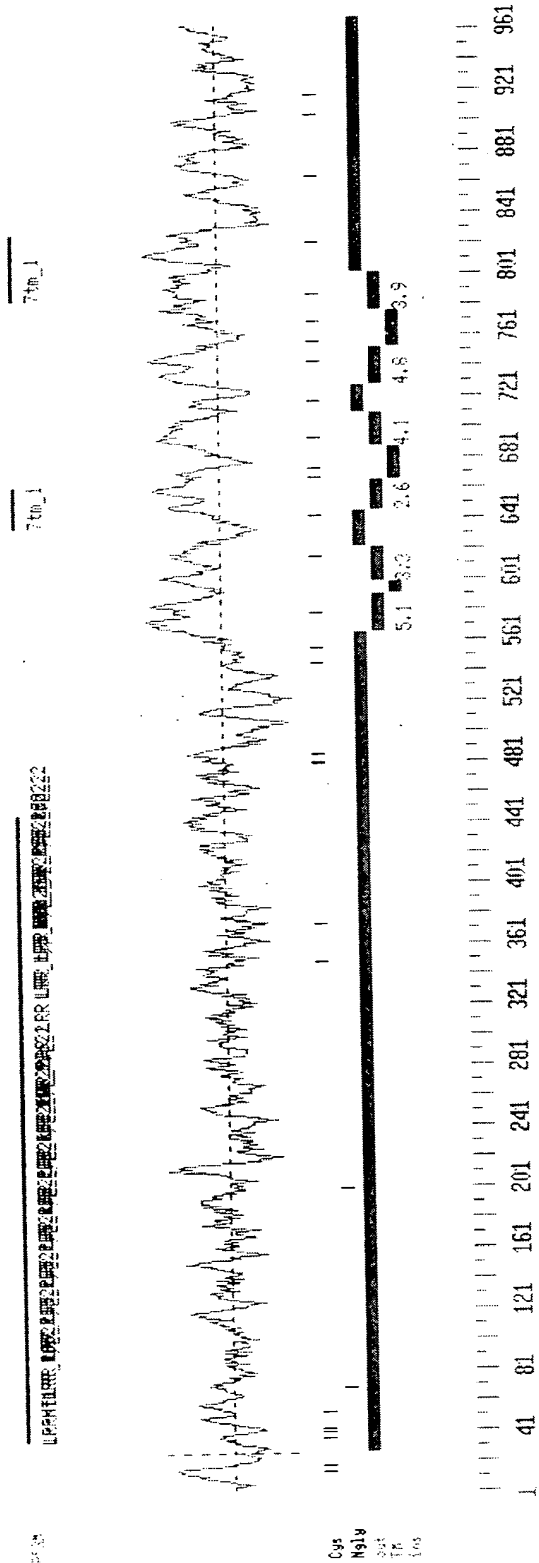


FIGURE 9

Searching for complete domains in PFAM
 hmmpfam - search a single seq against HMM database
 HMMER 2.1.1 (Dec 1998)
 Copyright (C) 1992-1998 Washington University School of Medicine
 HMMER is freely distributed under the GNU General Public License (GPL).

HMM file: /prod/ddm/seqanal/PFAM/pfam6.2/Pfam
 Sequence file: /prod/ddm/wspace/orfanal/oa-script.12184.seq

Query: 15088

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
LRR	Leucine Rich Repeat	241.4	1.3e-68	16
LRRNT	Leucine rich repeat N-terminal domain	27.2	0.00038	1
7tm_1	7 transmembrane receptor (rhodopsin family)	7.2	0.14	2

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
LRRNT	1/1	34	65	1	31	27.2	0.00038
LRR	1/16	67	90	1	23	12.4	11
LRR	2/16	91	114	1	23	24.2	0.0031
LRR	3/16	115	138	1	23	19.9	0.062
LRR	4/16	139	162	1	23	16.4	0.7
LRR	5/16	163	186	1	23	27.5	0.00031
LRR	6/16	187	210	1	23	12.1	13
LRR	7/16	211	234	1	23	21.6	0.019
LRR	8/16	235	257	1	23	18.2	0.2
LRR	9/16	258	281	1	23	19.0	0.11
LRR	10/16	282	305	1	23	10.2	32
LRR	11/16	306	328	1	23	5.6	1.5e+02
LRR	12/16	329	352	1	23	8.8	52
LRR	13/16	353	374	1	23	19.2	0.097
LRR	14/16	375	398	1	23	16.9	0.49
LRR	15/16	399	422	1	23	23.7	0.0042
LRR	16/16	423	446	1	23	16.4	0.66
7tm_1	1/2	635	662	51	79	3.4	2.2
7tm_1	2/2	784	827	207	259	1.1	11

Alignments of top-scoring domains:

LRRNT: domain 1 of 1, from 34 to 65: score 27.2, E = 0.00038
 ->aCpreCtCsp..fglvVdCsrgLtlevPrdIP<-
 aCp++C+C +++ l+ dCs++gL +vP dl
 15088 34 ACPAPCHCQEEdgIMLSADCSELGLS-AVPGDLD 65

LRR: domain 1 of 16, from 67 to 90: score 12.4, E = 11
 ->nLeeLdLsnN.LtspgglfsnLp<-
 +LdLs N+L+l pglf++L+
 15088 67 LTAYLDLSMNnLTELQPGLFHHLR 90

LRR: domain 2 of 16, from 91 to 114: score 24.2, E = 0.0031
 ->nLeeLdLsnN.LtspgglfsnLp<-
 LeeL+Ls+N+L+++p +fs+L
 15088 91 FLEELRLSGNhLSHIPGQAFSGLY 114

LRR: domain 3 of 16, from 115 to 138: score 19.9, E = 0.062
 ->nLeeLdLsnN.LtspgglfsnLp<-
 +L+ L L+nN+L ++p +++ Lp
 15088 115 SLKILMLQNNqLGGIPAEALWELP 138

LRR: domain 4 of 16, from 139 to 162: score 16.4, E = 0.7
 ->nLeeLdLsnN.LtspgglfsnLp<-
 +L++L+L+ N ++ +p+ +f++L+
 15088 139 SLQSLRLDANIISLVPERSFEGLS 162

LRR: domain 5 of 16, from 163 to 186: score 27.5, E = 0.00031
 ->nLeeLdLsnN.LtspgglfsnLp<-
 +L++L+L++N Lt++p +++nLp

FIGURE 10

15088 163 SLRHLWLDDNaLTEIPVRALNNLP 186

LRR: domain 6 of 16, from 187 to 210: score 12.1, E = 13
 ->nLeeLdLsnN.LtslppglfsnLp<-
 L+ L N++++p+ +f+nL+
 15088 187 ALQAMTLALNriSHIPDYAFQNLT 210

LRR: domain 7 of 16, from 211 to 234: score 21.6, E = 0.019
 ->nLeeLdLsnN.LtslppglfsnLp<-
 +L +L+L+nN++++l ++f++L
 15088 211 SLVVHLHLHNNrIQHLGTHSFEGH 234

LRR: domain 8 of 16, from 235 to 257: score 18.2, E = 0.2
 ->nLeeLdLsnN.LtslppglfsnLp<-
 nLe+LdL++N+L+++p +++ L
 15088 235 NLETDLNLYNkLQEFV-AIRTLG 257

LRR: domain 9 of 16, from 258 to 281: score 19.0, E = 0.11
 ->nLeeLdLsnN.LtslppglfsnLp<-
 +L+eL ++nN+++ +p+++f+ p
 15088 258 RLQELGFHNNnKAIPEKAFMGNP 281

LRR: domain 10 of 16, from 282 to 305: score 10.2, E = 32
 ->nLeeLdLsnN.LtslppglfsnLp<-
 L++++ +N+++ + ++f+ Lp
 15088 282 LLQTIHFYDNpIQFVGRSAFYLP 305

LRR: domain 11 of 16, from 306 to 328: score 5.6, E = 1.5e+02
 ->nLeeLdLsnN.LtslppglfsnLp<-
 +L++L+L++ +++++p+ +++ +
 15088 306 KLHTLSLNGAmdIQEFPD--LKGTT 328

LRR: domain 12 of 16, from 329 to 352: score 8.8, E = 52
 ->nLeeLdLsnN.LtslppglfsnLp<-
 +Le L L + +++ lp+g +++Lp
 15088 329 SLEILTLTRAgIRLLPSGMCQQLP 352

LRR: domain 13 of 16, from 353 to 374: score 19.2, E = 0.097
 ->nLeeLdLsnN.LtslppglfsnLp<-
 +L++L Ls+N++++lp+ ++ ++
 15088 353 RLRVLELSHNqIEELPS--LHRCQ 374

LRR: domain 14 of 16, from 375 to 398: score 16.9, E = 0.49
 ->nLeeLdLsnN.LtslppglfsnLp<-
 +Lee+ L++N+++ ++fs+L+
 15088 375 KLEEIGLQHNrWEIGADTFSQLS 398

LRR: domain 15 of 16, from 399 to 422: score 23.7, E = 0.0042
 ->nLeeLdLsnN.LtslppglfsnLp<-
 +L+ LdLs N ++s+++p++fs L
 15088 399 SLQALDLSWNaIRSIHPEAFSTLH 422

LRR: domain 16 of 16, from 423 to 446: score 16.4, E = 0.66
 ->nLeeLdLsnN.LtslppglfsnLp<-
 +L +LdL +N+L+lp ++L
 15088 423 SLVKLDLTDNqLTTPLAGLGGLM 446

7tm_1: domain 1 of 2, from 635 to 662: score 3.4, E = 2.2
 ->dWpfGsalCklvtaldvvnmyaSillLta<-
 +W G ++C+ +++l v+ + aS+lLl+
 15088 635 RWETG-LGCRATGFLAVLGSEASVLLLT 662

7tm_1: domain 2 of 2, from 784 to 827: score 1.1, E = 11
 *->ICWlPyfivllldtlc.lsiimsstCelervlptalvtwLayvNs
 l+ P+++ +l ++ ++++++v l++ ++
 15088 784 LLYCPVAFLSFASMLGIFV-----TPEAVKSVLLVVLPLPA 820

cINPiY<-*
 cINP++Y
 15088 821 CLNPLLY 827

FIGURE 10 cont.

```
//
Searching for complete domains in SMART
hmmpfam - search a single seq against HMM database
HMMER 2.1.1 (Dec 1998)
Copyright (C) 1992-1998 Washington University School of Medicine
HMMER is freely distributed under the GNU General Public License (GPL).
```

```
-----
HMM file:          /ddm/robison/smart/smart/smart.all.hmms
Sequence file:     /prod/ddm/wspace/orfanal/oa-script.12184.seq
-----
```

Query: 15088

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
LRR_typ_2		247.2	2.3e-70	14
LRR_PS_2		78.1	1.8e-19	13
LRR_sd22_2		33.5	4.9e-06	5
lrrntl		25.7	0.0011	1
LRR_bac_2		11.8	3	7
LRR_RI_2		5.4	7.7	4

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
lrrntl	1/1	34	70	1	38	25.7	0.0011
LRR_PS_2	1/13	64	87	1	24	1.9	1.2e+02
LRR_typ_2	1/14	64	88	1	24	12.6	2.1
LRR_bac_2	1/7	89	108	1	20	0.9	80
LRR_PS_2	2/13	89	111	1	24	17.2	0.4
LRR_typ_2	2/14	89	112	1	24	32.1	1.3e-05
LRR_RI_2	1/4	89	115	1	28	3.6	14
LRR_bac_2	2/7	113	132	1	20	1.6	66
LRR_PS_2	3/13	113	136	1	24	1.1	1.5e+02
LRR_typ_2	3/14	113	136	1	24	19.2	0.1
LRR_bac_2	3/7	137	156	1	20	0.1	1e+02
LRR_PS_2	4/13	137	159	1	24	7.1	24
LRR_typ_2	4/14	137	160	1	24	25.9	0.00095
LRR_PS_2	5/13	161	183	1	24	11.4	6.6
LRR_typ_2	5/14	161	184	1	24	27.5	0.00031
LRR_sd22_2	1/5	161	187	1	22	5.3	31
LRR_RI_2	2/4	161	190	1	28	5.3	8
LRR_PS_2	6/13	185	207	1	24	7.0	25
LRR_typ_2	6/14	185	208	1	24	23.2	0.0062
LRR_PS_2	7/13	209	232	1	24	3.1	79
LRR_typ_2	7/14	209	232	1	24	28.1	0.0002
LRR_RI_2	3/4	209	235	1	28	1.2	31
LRR_sd22_2	2/5	209	235	1	22	13.5	3
LRR_bac_2	4/7	233	252	1	20	10.7	4.1
LRR_typ_2	8/14	233	255	1	24	16.1	0.76
LRR_PS_2	8/13	233	255	1	24	17.1	0.43
LRR_bac_2	5/7	256	275	1	20	0.2	1e+02
LRR_PS_2	9/13	256	278	1	24	2.9	85
LRR_typ_2	9/14	256	279	1	24	24.4	0.0026
LRR_typ_2	10/14	327	350	1	24	3.1	29
LRR_bac_2	6/7	351	370	1	20	14.6	1.3
LRR_PS_2	10/13	351	372	1	24	10.8	8
LRR_sd22_2	3/5	351	372	1	22	7.6	16
LRR_typ_2	11/14	351	373	1	24	18.8	0.13
LRR_RI_2	4/4	351	378	1	28	2.6	19
LRR_PS_2	11/13	373	396	1	24	2.3	1e+02
LRR_typ_2	12/14	374	396	1	24	6.8	10
LRR_sd22_2	4/5	397	418	1	22	7.0	19
LRR_PS_2	12/13	397	419	1	24	13.6	3.4
LRR_typ_2	13/14	397	420	1	24	30.4	4.3e-05
LRR_bac_2	7/7	421	440	1	20	5.8	18
LRR_sd22_2	5/5	421	441	1	22	3.7	49
LRR_PS_2	13/13	421	442	1	24	5.5	39
LRR_typ_2	14/14	421	444	1	24	21.6	0.018

Alignments of top-scoring domains:

FIGURE 11

lrrnt1: domain 1 of 1, from 34 to 70: score 25.7, E = 0.0011
 ->qCPapCtCsp.dfgtaVdCsgrgLttlevPldlPadttl<-
 +CPapC+C ++ ++ dCs++gL +vP dl + t +
 15088 34 ACPAPCHCQEdGIMLSADCSELGLS--AVPGDLPLTAY 70

LRR_PS_2: domain 1 of 13, from 64 to 87: score 1.9, E = 1.2e+02
 ->LtsL.qvLdLsnNnLsGeIPsslgn<-
 L L+ +LdLs NnL+ e+ + l+
 15088 64 LDPLtAYLDLSMNNLT-ELQPGLFH 87

LRR_typ_2: domain 1 of 14, from 64 to 88: score 12.6, E = 2.1
 ->LpnL.reLdLsnNqLtsLPpgaFqg<-
 L L+ LdLs N+Lt+L pg+F++
 15088 64 LDPLtAYLDLSMNNLTTELQPGLFHH 88

LRR_bac_2: domain 1 of 7, from 89 to 108: score 0.9, E = 80
 ->PpsLkeLnvsnNrLteLPeL<-
 +LeL+ s+N+L+ P
 15088 89 LRFLEELRLSGNHLSHIPGQ 108

LRR_PS_2: domain 2 of 13, from 89 to 111: score 17.2, E = 0.4
 ->LtsLqvLdLsnNnLsGeIPsslgn<-
 L+ L++L+Ls+N+Ls +IP + ++
 15088 89 LRFLEELRLSGNHLs-HIPGQAFS 111

LRR_typ_2: domain 2 of 14, from 89 to 112: score 32.1, E = 1.3e-05
 ->LpnLreLdLsnNqLtsLPpgaFqg<-
 L+ L+eL+Ls+N+L+++P +aF+g
 15088 89 LRFLEELRLSGNHLSHIPGQAFSG 112

LRR_RI_2: domain 1 of 4, from 89 to 115: score 3.6, E = 14
 ->npsLreLdLsnNkl.gdeGaraLaeaLks<-
 ++ L+eL+Ls+N+l+++ G + ++L s
 15088 89 LRFLEELRLSGNHLSHIPG--QAFSGLYS 115

LRR_bac_2: domain 2 of 7, from 113 to 132: score 1.6, E = 66
 ->PpsLkeLnvsnNrLteLPeL<-
 sLk+L +nN+L P+
 15088 113 LYSLKILMLQNNQLGGIPAE 132

LRR_PS_2: domain 3 of 13, from 113 to 136: score 1.1, E = 1.5e+02
 ->LtsLqvLdLsnNnLsGeIPsslgn<-
 L sL++L L+nN+L G + l+
 15088 113 LYSLKILMLQNNQLGGIPAEALWE 136

LRR_typ_2: domain 3 of 14, from 113 to 136: score 19.2, E = 0.1
 ->LpnLreLdLsnNqLtsLPpgaFqg<-
 L +L+ L L+nNqL +P++a++
 15088 113 LYSLKILMLQNNQLGGIPAEALWE 136

LRR_bac_2: domain 3 of 7, from 137 to 156: score 0.1, E = 1e+02
 ->PpsLkeLnvsnNrLteLPeL<-
 psL++L+ + N ++ Pe
 15088 137 LPSLQSLRLDANLISLVPER 156

LRR_PS_2: domain 4 of 13, from 137 to 159: score 7.1, E = 24
 ->LtsLqvLdLsnNnLsGeIPsslgn<-
 L+sLq+L+L N +s +P+ +
 15088 137 LPSLQSLRLDANLIS-LVPERSFE 159

LRR_typ_2: domain 4 of 14, from 137 to 160: score 25.9, E = 0.00095
 ->LpnLreLdLsnNqLtsLPpgaFqg<-
 Lp+L++L+L+ N ++ +P++ F+g
 15088 137 LPSLQSLRLDANLISLVPERSFEG 160

LRR_PS_2: domain 5 of 13, from 161 to 183: score 11.4, E = 6.6
 ->LtsLqvLdLsnNnLsGeIPsslgn<-
 L+sL++L L +N L+ eIP n
 15088 161 LSSLRHLWLDNALT-EIPVRALN 183

LRR_typ_2: domain 5 of 14, from 161 to 184: score 27.5, E = 0.00031

FIGURE 11 cont.

->LpnLreLdLsnNqLtsLPpgaFqg<-
 L++Lr+L L++N+Lt++P +a+++
 15088 161 LSSLRHLWLDDNALTEIPVRALNN 184
 LRR_sd22_2: domain 1 of 5, from 161 to 187: score 5.3, E = 31
 ->LtnLeeLdLsqNkI.....kkiENLde<-
 L+ L++L+L +N +++ + + NL
 15088 161 LSSLRHLWLDDNALteipvRALNNLPA 187
 LRR_RI_2: domain 2 of 4, from 161 to 190: score 5.3, E = 8
 ->npsLreLdLsnNklgdeGaraL..aeaLks<-
 ++sLr L+L +N l++ +raL++ aL++
 15088 161 LSSLRHLWLDDNALTEIPVRALnnLPALQA 190
 LRR_PS_2: domain 6 of 13, from 185 to 207: score 7.0, E = 25
 ->LtsLqvLdLsnNnLsGeIPsslgN<-
 L+ Lq L+ N++s +IP+ ++
 15088 185 LPALQAMTLALNRIS-HIPDYAFQ 207
 LRR_typ_2: domain 6 of 14, from 185 to 208: score 23.2, E = 0.0062
 ->LpnLreLdLsnNqLtsLPpgaFqg<-
 Lp+L+ L N+++++P+ aFq+
 15088 185 LPALQAMTLALNRISHIPDYAFQN 208
 LRR_PS_2: domain 7 of 13, from 209 to 232: score 3.1, E = 79
 ->LtsLqvLdLsnNnLsGeIPsslgN<-
 LtsL+vL+L+nN++ s+
 15088 209 LTSLVVLHLHNNRIQHLGTHSFEG 232
 LRR_typ_2: domain 7 of 14, from 209 to 232: score 28.1, E = 0.0002
 ->LpnLreLdLsnNqLtsLPpgaFqg<-
 L++L +L+L+nN++++L F+g
 15088 209 LTSLVVLHLHNNRIQHLGTHSFEG 232
 LRR_RI_2: domain 3 of 4, from 209 to 235: score 1.2, E = 31
 ->npsLreLdLsnNklgdeGaraLaeaLks<-
 ++sL +L+L nN + G + e+L+
 15088 209 LTSLVVLHLHNNRIQHLGTHSF-EGLHN 235
 LRR_sd22_2: domain 2 of 5, from 209 to 235: score 13.5, E = 3
 ->LtnLeeLdLsqNkI.....kkiENLde<-
 Lt L++L L +N+I++ +++++E+L++
 15088 209 LTSLVVLHLHNNRIqhlgtHSFEGLHN 235
 LRR_bac_2: domain 4 of 7, from 233 to 252: score 10.7, E = 4.1
 ->PpsLkeLnvsnNrLteLPeL<-
 ++L++L+ ++N+L e+P
 15088 233 LHNLETLDLNYNKLQEFPA 252
 LRR_typ_2: domain 8 of 14, from 233 to 255: score 16.1, E = 0.76
 ->LpnLreLdLsnNqLtsLPpgaFqg<-
 L+nL++LdL++N+L++ P + +
 15088 233 LHNLETLDLNYNKLQEFPAI-RT 255
 LRR_PS_2: domain 8 of 13, from 233 to 255: score 17.1, E = 0.43
 ->LtsLqvLdLsnNnLsGeIPsslgN<-
 L++L++LdL++N+L e+P +
 15088 233 LHNLETLDLNYNKLQ-EFPVAIRT 255
 LRR_bac_2: domain 5 of 7, from 256 to 275: score 0.2, E = 1e+02
 ->PpsLkeLnvsnNrLteLPeL<-
 +LteL+ nN+++ Pe
 15088 256 LGRLQELGFHNNNIKAIPK 275
 LRR_PS_2: domain 9 of 13, from 256 to 278: score 2.9, E = 85
 ->LtsLqvLdLsnNnLsGeIPsslgN<-
 L +Lq+L ++nNn+ IP+ +
 15088 256 LGRLQELGFHNNNIK-AIPEKAFFM 278
 LRR_typ_2: domain 9 of 14, from 256 to 279: score 24.4, E = 0.0026
 ->LpnLreLdLsnNqLtsLPpgaFqg<-

FIGURE 11 cont.

L+ L+eL +nN++++P+ aF g
 15088 256 LGRLQELGFHNNNIKAIPKAFMG 279
 LRR_typ_2: domain 10 of 14, from 327 to 350: score 3.1, E = 29
 ->LpnLreLdLsnNqLtsLPpgaFqg<-
 ++L+ L L + ++ LP+g++q
 15088 327 TTSLEILTLAGIRLLPSGMCQQ 350
 LRR_bac_2: domain 6 of 7, from 351 to 370: score 14.6, E = 1.3
 ->PpsLkeLnvsNnrLteLPeL<-
 p+L+ L s+N+++eLP L
 15088 351 LPRLRVLELSHNQIEELPSL 370
 LRR_PS_2: domain 10 of 13, from 351 to 372: score 10.8, E = 8
 ->LtsLqvLdLsnNnLsGeIPsslgN<-
 L++L+vL+Ls+N++ e+Ps l +
 15088 351 LPRLRVLELSHNQIE-ELPS-LHR 372
 LRR_sd22_2: domain 3 of 5, from 351 to 372: score 7.6, E = 16
 ->LtnLeeLdLsqNkIkkiENLde<-
 L +L++L+Ls+N+I+ + L+
 15088 351 LPRLRVLELSHNQIEELPSLHR 372
 LRR_typ_2: domain 11 of 14, from 351 to 373: score 18.8, E = 0.13
 ->LpnLreLdLsnNqLtsLPpgaFqg<-
 Lp Lr+L Ls+Nq++LP + ++:
 15088 351 LPRLRVLELSHNQIEELP-SLHRC 373
 LRR_RI_2: domain 4 of 4, from 351 to 378: score 2.6, E = 19
 ->npsLreLdLsnNklgdeGaraLaealks<-
 +p+Lr+L Ls+N + + + ++ L++
 15088 351 LPRLRVLELSHNQIEELPSLHRCQKLEE 378
 LRR_PS_2: domain 11 of 13, from 373 to 396: score 2.3, E = 1e+02
 ->LtsLqvLdLsnNnLsGeIPsslgN<-
 +++L+++ L++N++ +++++
 15088 373 CQKLEEIGLQHNRIWEIGADTFSQ 396
 LRR_typ_2: domain 12 of 14, from 374 to 396: score 6.8, E = 10
 ->LpnLreLdLsnNqLtsLPpgaFqg<-
 +L+e L++N++ ++ ++F+
 15088 374 -QKLEEIGLQHNRIWEIGADTFSQ 396
 LRR_sd22_2: domain 4 of 5, from 397 to 418: score 7.0, E = 19
 ->LtnLeeLdLsqNkIkkiENLde<-
 L+ L+ LdLs+N I++i
 15088 397 LSSLQALDLSWNAIRSIHPEAF 418
 LRR_PS_2: domain 12 of 13, from 397 to 419: score 13.6, E = 3.4
 ->LtsLqvLdLsnNnLsGeIPsslgN<-
 L+sLq LdLs+N + +I ++ ++
 15088 397 LSSLQALDLSWNAIR-SIHPEAFS 419
 LRR_typ_2: domain 13 of 14, from 397 to 420: score 30.4, E = 4.3e-05
 ->LpnLreLdLsnNqLtsLPpgaFqg<-
 L++L+ LdLs+N+++++p+aF+
 15088 397 LSSLQALDLSWNAIRSIHPEAFST 420
 LRR_bac_2: domain 7 of 7, from 421 to 440: score 5.8, E = 18
 ->PpsLkeLnvsNnrLteLPeL<-
 +sL +L+ +N+Lt+LP
 15088 421 LHSLVKLDLTDNQLTTLPLA 440
 LRR_sd22_2: domain 5 of 5, from 421 to 441: score 3.7, E = 49
 ->LtnLeeLdLsqNkIkkiENLde<-
 L+ L+ LdL +N+++ + L +
 15088 421 LHSLVKLDLTDNQLTTL-PLAG 441
 LRR_PS_2: domain 13 of 13, from 421 to 442: score 5.5, E = 39
 ->LtsLqvLdLsnNnLsGeIPsslgN<-
 L+sL+ LdL +N+L+ ++P g

FIGURE 11 cont.

```

15088  421  LHSLVKLDLTDNQLT-TLPL-AGL      442
LRR_typ_2: domain 14 of 14, from 421 to 444: score 21.6, E = 0.018
          *->LpnLreLdLsnNqLtsLPpgaFqg<-*
          L++L +LdL +NqLt+LP      ++g
15088  421  LHSLVKLDLTDNQLTTLPLAGLGG      444
//

```

FIGURE 11 cont.

[illegible]

to: FrGcgManager_101_ITA0fLsO_ check: 3059 from: 1 to: 2711

Symbol comparison table:

CompCheck: 8760

Quality:	21826	Length:	3688
Ratio:	8.051	Gaps:	20
Percent Similarity:	84.248	Percent Identity:	84.211

| = IDENTITY

$$: = 5$$
$$\cdot = 1$$

901 CCCACAGCTTCGAGGGGCTGCACAATCTGGAGACACTAGACCTGAACTAT 950 MOUSE

|||||

1GGGCTGCACAATCTGGAGACACTAGACCTGAATTAT 36 HUMAN

951 AATGAGCTGCAGGAGTTCCCCTTGGCTATCCGGACCCTGGGCAGACTGCA 1000

|| |||||

37 AACAAAGCTGCAGGAGTTCCCTGTGGCCATCCGGACCCTGGGCAGACTGCA 86

1001 AGAATTGGGTTTCCATAACAACAACATCAAGGCTATCCCAGAGAAAGCCT 1050

001	0001	0000	1100	1110	1010	1011	1101	1111	1001	1000	0000	0001	0010	0011	0100	0101	0110	0111	1000	1001	1010	1011	1100	1101	1110	1111	0000	0001	0010	0011	0100	0101	0110	0111	1000	1001	1010	1011	1100	1101	1110	1111
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87 GGAAGTGGGGTTCATAACAACAACATCAAGGCCATCCCAGAAAAGGCCT 136

1051 TCATGGGCAACCCTCTCCTGCAGACAATACATTTTATGACAACCCAATC 1100

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	5
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137 TCATGGGGAACCCTCTGCTACAGACGATACACTTTTATGATAACCCAATC 186

1101 CAGTTTGTGGGAAGGTCAGCATTCCAGTACCTGTCTAAACTGCATACGCT 1150

[illegible]

187 CAGTTTGTGGGAAGATCGGCATTCCAGTACCTGCCTAAACTCCACACACT 236

1151 ATCTTTGAATGGTGCCACTGATATCCAAGAGTCCCAGACCTCAAAGGCA 1200

[illegible]

237 ATCTCTGAATGGTGCCATGGACATCCAGGAGTTTCCAGATCTCAAAGGCA 286

1201 CCACTAGCCTGGAGATCCTGACCCTGACCCGTGCGGGGCATCAGACTGCTC 1250

[illegible]

287 CCACCAGCCTGGAGATCCTGACCCTGACCCGCGCAGGCATCCGGCTGCTC 336

1251 CCACCGGGAGTGTGCCAACAGCTGCCTAGGCTCCGAATCCTGGAGCTGTC 1300

||||| ||||| |

337 CCATCGGGGATGTGCCAACAGCTGCCCAGGCTCCGAGTCCTGGAACTGTC 386

FIGURE 12

2801 GAAGAGCTCCTGCGACTCCACCCAAGCGCTGGTGGCTTTCTCAGATGTGG 2850
 ||||| || || ||||| || ||||| || ||||| |||||
 1887 GAAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGG 1936
 2851 ATCTTATTCTGGAAGCTTCTGAGGCTGGGCAGCCTCCTGGGCTAGAGACC 2900
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1937 ATCTCATTCTGGAAGCTTCTGAAGCTGGGCGGCCCTGGGCTGGAGACC 1986
 2901 TATGGCTTCCCTTCAGTGACCCCTCATCTCCCGACATCAGCCGGGGGCCAC 2950
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1987 TATGGCTTCCCTTCAGTGACCCCTCATCTCCTGTGAGCAGCCAGGGGCCCC 2036
 2951 CAGGCTGGAGGGAAACCATTTTATAGAGTCTGATGGAACCAAGTTTGGGA 3000
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2037 CAGGCTGGAGGGCAGCCATTGTGTAGAGCCAGAGGGGAACCACTTTGGGA 2086
 3001 ACCCACAACCTCCCATGAAGGGGAGAACTGCTGCTGAAGGCAGAGGGAGCC 3050
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2087 ACCCCCAACCTCCATGGATGGAGAACTGCTGCTGAGGGCAGAGGGATCT 2136
 3051 ACTTTGGCAGGCTGTGGCTCTTCCGTGGGTGGAGCCCTCTGGCCCTCTGG 3100
 || ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2137 ACGCCAGCAGGTGGAGGCTTGTGAGGGGTGGCGGCTTTAGCCCTCTGG 2186
 3101 CTCTCTCTTTGCCTCTCACTTGTAATATCCCT..... 3133
 || ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2187 CTTGGCCTTTGCTTCACACGTGTAATATCCCTCCCCATTCTTCTCTTCC 2236
 3134 .CTCTGTT...TGTC..CTCTCCCCATC...CAATGATGGCTGCTTATAA 3174
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2237 CCTCTCTTCCCTTTCTCTCTCCCCCTCGGTGAATGATGGCTGCTTCTAA 2286
 3175 AAGAAAGACAACCTCCAAC.....TCCATAGCAAGATGGCCAAC 3212
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2287 AACAAATACAACCAAACTCAGCAGTGTGATCTATAGCAGGATGGCCAG 2336
 3213 ACCTCTGACTCCATTGTT...CTCTCTCCACGACCCCTAACCAATGAGTG 3259
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2337 TAC.CTGGCTCCACTGATCACCTCTCTCCTGTGACCATCACCAACGGGTG 2385
 3260 CTTCCAAGTCTTGCTTTGTCTTGGCCT...TCAGCTTCACTTTACCCCTG 3306
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2386 CCTCTTGGCCTGGCTTTCCCTTGGCCTTCCTCAGCTTACCTTGATACTG 2435
 3307 GGC...CTTCTCTGTCCAATCCAATACTTCTGA.CAGAGGCCTGGGAAATT 3353
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2436 GGCCTCTTCCTTGTCTGATGTCTGAAGCTGTGGACCAGAGACCTGGACTTTT 2485
 3354 ...TGCATAGGAGAAAGGAGAAAAGCAAAAGACAGTGAAGGTTATTGGGC 3400
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2486 GTCTGCTTAAGGGAAATGAGGGAAG.TAAAGACAGTGAAG.....GGG. 2527
 3401 CCTGACAGAGCCATGATCAGTAAGTGCAGAGT.GATGGGGAGGTCTCACA 3449
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2528 ..TG...GAGGGTTGATC....AGGGCACAGTGGACAGGGAGACCTCACA 2568
 3450 GAGCATGACACTGGAAGACAACCTACCAAAGACATTGGAGAGTCTCCCCTG 3499
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2569 GAGAAAGGC.CTGAAGGTGATTTCC.....CGTGTGACTC..... 2603

FIGURE 12
 CONT.

1. The first part of the paper is devoted to the study of the asymptotic behavior of the solutions of the system (1) as $\epsilon \rightarrow 0$. It is shown that the solutions of the system (1) converge to the solutions of the system (2) in the sense of the weak convergence in the space $L^2(\Omega; \mathbb{R}^n)$.

CONT .

GAP of: FrGcgManager_102_MTA0uXMaE check: 8470 from: 1 to: 968

mLGR6.aa (analysis only) - Import - complete

to: FrGcgManager_102_NTAf7nC1_ check: 5092 from: 1 to: 737

corrected hLGR6.aa (analysis onl - Import - complete

Symbol comparison table: /prod/ddm/seqanal/BLAST/matrix/aa/BLOSUM62

CompCheck: 1102

Matrix made by matblas from blosum62.iiij

Gap Weight: 12 Average Match: 2.778
Length Weight: 4 Average Mismatch: -2.248

Quality: 3424 Length: 968
Ratio: 4.646 Gaps: 0
Percent Similarity: 90.773 Percent Identity: 89.281

Match display thresholds for the alignment(s):

| = IDENTITY

: = 2

. = 1

FrGcgManager_102_MTA0uXMaE x FrGcgManager_102_NTAf7nC1_

201 IPDYAFQNLTSLVVLHLHNNRIQHVGTSHFEGLHNLETLDLNYNELQEFF 250 MOUSE
1GLHNLETLDLNYNKLQEFF 19 HUMAN
251 LAIRTLGRQLQELGFHNNNIKAIPEKAFMGNPLLQTIHFYDNPIQFVGRSA 300
20 VAIRTLGRQLQELGFHNNNIKAIPEKAFMGNPLLQTIHFYDNPIQFVGRSA 69
301 FQYLSKLHTLSLNGATDIQEFDPDLKGTTSLEILTLTRAGIRLLPPGVCQQ 350
70 FQYLPKLHTLSLNGAMDIEFPDLKGTTSLEILTLTRAGIRLLPSGMCQQ 119
351 LPRLRILELSHNQIEELPSLHRCQKLEEIGLRHNRIKEIGADTFSQLGSL 400
120 LPRLRVLELSHNQIEELPSLHRCQKLEEIGLQHNRIWEIGADTFSQLSSL 169
401 QALDLSWNAIRAIHPEAFSTLRSVLKDLTDNQLTTPLAGLGGLMHLKL 450
170 QALDLSWNAIRSIHPEAFSTLHSLVKDLTDNQLTTPLAGLGGLMHLKL 219
451 KGNLALSQAFSKDSFPKLRILEVPYAYQCCAYGICASFFKTSGQWQAEDF 500
220 KGNLALSQAFSKDSFPKLRILEVPYAYQCCPYGMCASFFKASGQWEAEDL 269
501 HPEEEEEAPKRPLGLLAGQAENHYDLDLDELQMGTEDSKPNPSVQCSPVPG 550
270 HLDDEESSKRPLGLLARQAENHYDQDLDELQLEMEDSKPHPSVQCSPTPG 319
551 PFKPCEHLFESWGIRLAVWAIVLLSVLCNGLVLLTVFASGPSPLSPVKLV 600
320 PFKPCEYLFESWGIRLAVWAIVLLSVLCNGLVLLTVFAGGPAPLPPVKFV 369

FIGURE 13

>15088
> Fbh150881 - Import - vector trimmed
CCGCCSGCGGTGCAGCCCGCCGGGACCGGGAGGCGGCAGCTGCGGCCACCGCGCCGTGCG
TCCGCGCCCGGCCCGCCAGGTGCCCGAGTAGCCCGACCGCCGAGATGCCAGCCCGCCGGG
GCTCCGGGCGCTATGGCTTTGCGCCGCGCTGTGCGCTTCCCGGAGGGCCGCGCGGCCCC
CCAGCCCGGGCCCGGGGCCACCGCCTGCCCGGCCCCCTGCCACTGCCAGGAGGACGGCAT
CATGCTGTCTGCCGACTGCTCTGAGCTCGGGCTGTCCGCCGTTCCGGGGGACCTGGACCC
CCTGACGGCTTACCTGGACCTCAGCATGAACAACCTCACAGAGCTTCAGCCTGGCCTCTT
CCACCACCTGCGCTTCTTGAGGAGCTGCGTCTCTTGGAACCATCTCTCACACATCCC
AGGACAAGCATTCTCTGGTCTCTACAGCCTGAAAACTCTGATGCTGCAGAACAATCAGCT
GGGAGGAATCCCCGAGAGGCGCTGTGGGAGCTGCCGAGCCTGCAGTCGCTGCGCCTAGA
TGCCAACTCATCTCCCTGGTCCCGGAGAGGAGCTTTGAGGGGCTGTCTCCCTCCCGCCA
CCTCTGGCTGGACGACAATGCACTCACGGAGATCCCTGTCAGGGCCCTCAACAACCTCCC
TGCCCTGCAGGCCATGACCCTGGCCCTCAACCGCATCAGCCACATCCCCGACTACGCGTT
CCAGAATCTCACCAGCCTTGTGGTGTGCAATTTGCATAACAACCGCATCCAGCATCTGGG
GACCCACAGCTTCGAGGGGCTGCACAATCTGGAGACACTAGACCTGAATTATAACAAGCT
GCAGGATCTCCCTGTGGCCATCCGGACCTGGGCAGACTGCAGGAACCTGGGGTTCCATAA
CAACAACATCAAGGCCATCCAGAAAAGGCCTTCATGGGGAACCTCTGCTACAGACGAT
ACACTTTTATGATAACCCAATCCAGTTTGTGGGAAGATCGGCATTCCAGTACCTGCCTAA
ACTCCACACACTATCTCTGAATGGTGCCATGGACATCCAGGAGTTTCCAGATCTCAAAGG
CACCACCGCCTGGAGATCCTGACCCTGACCCGCGCAGGCATCCGGCTGCTCCCATCGGG
GATGTGCCAACAGCTGCCAGGCTCCGAGTCTGGAACCTGTCTACAATCAAATTGAGGA
GCTGCCCAGCCTGCACAGGTGTGAGAAATTGGAGGAAATCGGCCCTCAACACAACCGCAT
CTGGGAAATTGGAGCTGACACCTTCAGCCAGCTGAGCTCCCTGCAAGCCCTGGATCTTAG
CTGGAACGCTTCCCTGGTCCATCCACCTGAGGCCTTCTCCACCCTGCACTCCCTGGTCAA
GCTGGACCTGACAGACAACAGCTGACCACACTGCCCTGGCTGGACTTGGGGGCTTGAT
GCATCTGAAGCTCAAAGGGAACCTTGTCTCTCCAGGCCCTTCTCCAAGGACAGTTTCCC
AAAAGTGAAGATCCTGGAGGTGCCTTATGCCTACCAGTGTGTCCCTATGGGATGTGTGC
CAGCTTCTTCAAGGCCTCTGGGCACTGGGAGGCTGAAGACCTTCACCTTGATGATGAGGA
GTCTTCAAAAAGGCCCTTGGGCCCTCCTTGCCAGACAAGCAGAGAACCACTATGACCAGGA
CCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAAAGCCACACCCCACTGTCCAGTGTAG
CCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCTCTTGAAGCTGGGGCATCCGCCT
GGCCGTGTGGGCCATCGTGTGCTCTCCGTGCTGCAATGGACTGGTGTGCTGCTGACCGT
GTTGCTGGCGGGCCTGCCCCCTGCCCGGCTCAAGTTTGTGGTAGGTGCGATTGCAGG
CGCCAACACCTTGACTGGCATTCTCTGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCTT
TGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGACCGGGCTAGGCTGCCGGGCCACTGG
CTTCTGGCAGTACTTGGGTCCGAGGCATCGGTGCTGCTGCTCACTTGGCCGCAATGCA
GTGCAAGCTCTCCGTCTCCTGTGTCCGGGCTATGGGAAGTCCCCCTCCCTGGGCAGCGT
TCGAGCAGGGGTCTAGGCTGCCTGGCACTGGCAGGGCTGGCCGCGCACTGCCCTGGC
CTCAGTGGGAGAATACGGGGCCTCCCCACTCTGCCCTGCCCTACGCGCCACCTGAGGGTCA
GCCAGCAGCCCTGGGCTTACCGTGGCCCTGGTGATGATGAACTCCTTCTGTTTCTGGT
CGTGGCCGCTGCTACATCAAAGTGTACTGTGACCTGCCGCGGGGCACTTTGAGGCCGT
GTGGGACTGCGCCATGGTGAGGCACGTGGCCTGGCTCATCTTCGACAGCGGGCTCCTCTA
CTGTCCCGTGGCCTTCTCAGCTTCGCTCCATGCTGGGCCTTCTCCCTGTACGCCCCGA
GGCCGTCAAAGTCTGTCTGCTGGTGGTGTGCTGCCCTGCCTGCCTGCCTCAACCACTGCT
GTACCTGCTCTTCAACCCCCACTTCCGGGATGACCTTCGGCGGCTTCGGCCCCGCGCAGG
GGACTCAGGGCCCCCTAGCCTATGCTGCGGCCGGGGAGCTGGAGAAGAGCTCCTGTGATTC
TACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCTCATTCTGGAAGCTTCTGAAGCTGG
GCGGCCCCCTGGGCTGGAGACCTATGGCTTCCCTCAGTGACCTCATCTCCTGTACGCA
GCCAGGGGCCCCAGGCTGGAGGGCAGCCATTGTGTAGAGCCAGAGGGGAACCACTTTGG
GAACCCCCAACCTCCATGGATGGAGAAGTGTGCTGAGGGCAGAGGGATCTACGCCAGC
AGGTGGAGGCTTGTACGGGGTGGCGGCTTTCAGCCCTCTGGCTTGGCCTTGTCTTACA
CGTGTAAATATCCCTCCCCATTCTTCTTCCCCTCTCTTCCCTTCTCTCCCCCTC
GGTGAATGATGGCTGCTTCTAAAACAAATACAACCAAACTCAGCAGTGTGATCTATAGC
AGGATGGCCCACTACCTGGCTCCACTGATCACCTCTCTCTGTGACCATCACCAACGGGT
GCCTCTTGGCCTGGCTTCCCTTGGCCTTCTCAGCTTACCTTGATACTGGGCCTCTTC
CTTGTCTATGTCTGAAGCTGTGGACCARAGACCTGGACTTTTGTCTGCTTAAGGGAAATGA
GGGAAGTAAAGACAGTGAAGGGGTGGAGGGTTGATCAGGGCACAGTGACAGGGAGACCT
CACARAAAAAGGCCTGGAAGGKATTTCCCGTGTGACTCATGGRTAGGAWACAAATGTG
TTCCATGTACCATTAATCTTGACATATGCCATGCATAAARACTTCTATTAAAATAAGCT
TTGGRAGAGATT

FIGURE 14

>15088

MPSPPLRALWLCAALCASRRAGGAPQPGPGPTACAPCHCQEDGIMLSADCSELGLSAVPGDLDPLTAYLDLSMNNLT
ELQPGLFHHLRFLEELRLSGNHLSHIPGQAFSGLYSLKILMLQNNQLGGIPAEALWELPSLQSLRLDANLISLVPERSFEGLS
SLRHLWLDNALTEIPVRALNNLPALQAMTLALNRISHIPDYAFQNLTSVLHLHNNRIQHLGTHSFEGHLNLETLDLNYNK
LQEFVVAIRTLGRLQELGFHNNNIKAIEKAFMGNPPLLQTIHFYDNPIQFVGRSAFYLPKLHTLSLNGAMDIQEPDLKGT
SLEILTLTRAGIRLLPSGMCQQLPRLRVLELSHNQIEELPSLHRCQKLEEIGLQHNRIWEIGADTFSQLSSLQALDLSWNAIR
SIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGMLHLKLKGNLALSQAFSKDSFPKLRILEVPYAYQCCPYGMCASFFKASG
QWEAEDLHLDDEESSKRPLGLLARQAENHYDQDLDELQLEMEDSKPHPSVQCSPTPGPFKPCFYLFEISWGIRLAWVAIVL
LSVLCNGLVLLTVFAGGPAPLPPVKFVVGAIAGANTLTGISCGLLASVDALTFGQFSEYGARWETGLGCRATGFLAVLGSE
ASVLLTLAAVQCSVSVSCVRAYGKSPSLGSRVAGVLGCLALAGLAAALPLASVGEYGASPLCLPYAPPEGQPAALGFTVA
LVMMNSFCFLVAGAYIKLYCDLPRGDFEAVWDCAMVRHVAWLIFADGLLYCPVAFLSFASMLGLFPVTPEAVKSULLVVL
PLPACLNPLLYLLFNPHFRDDLRLRPRAGDSGLAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGRPPGLETYGFP
SVTLISCQQPGAPRLEGSHCVEPEGNHFGNPQPSMDGELLRAEGSTPAGGGLSGGGGFQPSGLAFASHV*

FIGURE 15

